# CARACTERIZACIÓN GENÉTICA MOLECULAR Y VARIABILIDAD ESPACIALTEMPORAL DE POBLACIONES DE LA POLILLA DE LA MANZANA EN LA REGIÓN DEL MAULE

**ESTEBAN BASOALTO VENEGAS**
**DOCTOR EN CIENCIAS AGRARIAS**

## RESUMEN

Palabras clave: *Cydia pomonella*, microsatélites, kairomona, éster de pera, marcaje - captura, geo-estadística, variograma, kriging. Con el fin de estudiar la variabilidad espacial-temporal y la estructura genética de poblaciones de la polilla de la manzana, *Cydia pomonella* (Lepidoptera: Tortricidae), se seleccionaron dos huertos ubicados en agroecosistemas típicos de la zona central de Chile. En cada zona de estudio se definió un área de muestreo de 100 hectáreas, donde se ubicaron 50 trampas de feromona (codlemona) por huerto, considerando su entorno y zonas de acopio de bines. Estas trampas fueron georeferenciadas y revisadas periódicamente durante dos temporadas. Un análisis geoestadístico indica que las poblaciones de polilla de la manzana se distribuyen en forma agregada, tanto en elhuerto como en su entorno, produciendo fuentes de dispersión de polillas adultas dentro del paisaje. Con el objetivo de determinar efectivamente la dispersión de la plaga, estas fuentes poblacionales se marcaron durante la segunda temporada, mediante el uso de proteína de huevo, soya y leche. Luego se dispusieron 10 trampas adicionales con cebos de feromona y kairomona (éster de pera), capaces de atrapar machos y hembras adultas. Con posterioridad se identificó el origen de los individuos marcados con una prueba de inmuno-respuesta, específica para cada proteína, determinándose que existe dispersión de individuos adultos de *C. pomonella* entre el huerto con manejo y su entorno sin manejo para esta plaga. Además, se extrajo ADN de los individuos capturados en las trampas de feromona, de ambas temporadas, para su caracterización genética en espacio y tiempo mediante el uso de 5 marcadores moleculares microsatélites. Los análisis de varianza molecular (AMOVA) y las pruebas de asignamiento Bayesiano indican que la mayor parte de la variabilidad genética ocurre a nivel individual. Es así como no se encontró evidencia de estructura poblacional a escala espacial entre el huerto y el entorno, pero si se

detectó una pequeña estructura genética a través del tiempo al comparar entre generaciones y temporadas. Los resultados sugieren que la presión de selección impuesta, dentro de los huertos manejados con aplicaciones regulares de insecticidas, hacia el desarrollo de resistencia a los insecticidas de uso más frecuente contra *C. pomonella*, estaría balanceada por el flujo genético desde fuentes poblacionales del entorno no manejado. Por lo tanto, el conocimiento de la distribución espacial y estructura genética de la polilla de la manzana resultaría de gran importancia para el diseño de programas de manejo eficiente de esta plaga.

**ABSTRACT**

Key words: *Cydia pomonella*, microsatellites, kairomone, pear ester, marking - capture, geo-statistics, variogram, kriging.

In order to study the spatial-temporal variability and genetic structure of populations of the codling moth, *Cydia pomonella* (Lepidoptera: Tortricidae), two orchards located in typical agro-ecosystems from central Chile were selected. In each study zone we defined a sampling area of 100 hectares, where 50 pheromone (codlemone) traps per orchard were placed, considering the surroundings and bin pile zones. These traps were georeferenced and periodically served for two seasons. A geostatistical analysis indicated that the codling moth populations showed an aggregated distribution, both in the orchard and in its surroundings, producing dispersion sources of adult moths in the landscape. In order to effectively determine the dispersal of this pest, these population sources were marked during the second season with egg protein, soy and milk. Then 10 additional traps with pheromone and kairomone (pear ester) lures were placed, able of trapping adult males and females.Later the origin of marked individuals was identified with an immuno-response test, specific for each protein, determining that there is dispersal of *C. pomonella* adult individuals between the managed orchard and its surroundings without management for this pest. Furthermore, DNA from individuals captured in pheromone traps in both seasons was extracted for genetic characterization in space and time by using five microsatellite markers. The analysis of molecular variance (AMOVA) and Bayesian assignment tests indicate that the main part of genetic variability occurs at individual level. No evidence of population genetic structure at spatial scale, between the orchard and its surroundings was found. However, a significant small genetic structure over time between generations and seasons was detected. The results suggest that the selection pressure imposed, inside the orchards managed with regular insecticide sprays, for the development of resistance toward the insecticides most commonly used against *C. pomonella*, would be balanced by gene flow from unmanaged population sources in the surroundings. Therefore, knowledge of the spatial distribution and genetic structure of codling moth would be of great importance for the design of efficient management programs for this pest.

# LANDSCAPE ANALYSIS OF ADULT CODLING MOTH (LEPIDOPTERA: TORTRICIDAE) DISTRIBUTION AND DISPERSAL WITHIN TYPICAL AGROECOSYSTEMS DOMINATED BY APPLE PRODUCTION IN CENTRAL CHILE

## ABSTRACT

We analyzed the spatial distribution and dispersal of codling moth, *Cydia pomonella* (L.), adults within two heterogeneous agro-ecosystems typical of central Chile; commercial apple, *Malus domestica* Borkhausen, orchards surrounded by various unmanaged host plants. Both a geostatistical analysis of catches of adult males with a grid of sex pheromone-baited traps, and an immunological self-marking technique combined with traps baited with a male and female attractant were used. The spatial analyses identified the key sources of moths within these diverse landscapes. Codling moth catches in traps were spatially associated within distances of approx. 150 to 300 m. Similarly, the mean distance from the immunological self-marking plots within the commercial apple orchard to the traps which captured marked adults was 282 m. In contrast, the mean distance in the capture of marked moths from unmanaged selfmarking plots to a commercial orchard was 828 m. These data suggest that the success of any future areawide management programs for codling moth in Chilean pome fruit must include a component for managing or removing non-commercial hosts that surround orchards. This analysis also suggests that the selection pressure for resistance imposed by insecticide sprays within managed orchards is likely dampened by the influx of susceptible moths from unmanaged sites common in central Chile.

**Key Words**: geostatistics, immunomarking, mark-capture, areawide, *Cydia pomonella*

# SPATIAL AND TEMPORAL GENETIC VARIABILITY AND STRUCTURE IN POPULATIONS OF *CYDIA POMONELLA* FROM A HETEROGENEOUS AGRICULTURAL LANDSCAPE

## ABSTRACT

1.- Population genetic structure of the codling moth *Cydia pomonella* was evaluated in a heterogeneous agricultural landscape in central Chile. Samples of adult males were obtained from pheromone traps located inside or outside an insecticide managed orchard during the seasons 2006-2007 and 2007-2008.

2.- Genetic variability was evaluated with five microsatellite markers, which were used to assess the population genetic structure across space and time. Analysis of molecular variance (AMOVA) and Bayesian assignment tests did not found genetic structure on space, but a small but significant genetic structure between generations and season was detected.

3.- Adult dispersal between managed and unmanaged orchards has been previously shown for this species, which genetic consequences can now be observed in a lack of spatial structure on a landscape scale.

4.- Differences in genetic structure across time, between samples from different generations and seasons, could be related with insecticide management inside orchards that might be shaping the population genetic structure of this major pest of pome fruits worldwide.